

SEQUENCE LISTING

SEQ ID NO:1 p33ING2 polypeptide sequence

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1  MLGQQQQQLY SSAALLTGER SRLLTCTYVQD YLECVELPH DMQRNVSVLR
51  ELDNKYQETL KEIDDVYEKY KKEDDLNQKK RLQQLLQRAL INSQELGDEK
101 IQIVTQMLEL VENRARQMEL HSQCFQDPAE SERASDKAKM DSSQPERSSR
151 RPRRQRTSES RDLCHMANGI EDCDDQPPKE KKSksAKKKK RSKAKQEREA
201 SPVEFAIDPN EPTYCLCNQV SYGEMIGCDN EQCPIEFHF SCVSLTYKPK
251 GKWYCPKCRG DNEKTMKST ETKKDRRSR
    
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SEQ ID NO:2 p33ING2 Nucleic acid sequence

(GenBank Accession No. AF053537)

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1  gcggccgcgg cgggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcggt
61  cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg
121 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt
181 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaaga
241 aacgttaaag gaaattgatg atgtctacga aaaatataag aaagaagatg atttaaacca
301 gaagaaacgt ctacagcagc ttctccagag agcactaatt aatagtcaag aattgggaga
361 tgaaaaaata cagattgtta cacaatgct cgaattggtg gaaaatcggg caagacaaat
421 ggagttacac tcacagtgtt tccaagatcc tgctgaaagt gaacgagcct cagataaagc
481 aaagatggat tccagccaac cagaaagatc ttcaagaaga ccccgaggc agcggaccag
541 tgaaagccgt gatttatgtc acatggcaaa tgggattgaa gactgtgatg atcagccacc
601 taaagaaaag aaatccaagt cagcaaagaa aaagaaacgc tccaaggcca agcaggaaaag
661 ggaagcttca cctgttgagt ttgcaataga tcctaataa cctacatact gcttatgcaa
721 ccaagtgtct tatggggaga tgataggatg tgacaatgaa cagtgtccaa ttgaatggtt
781 tcacttttca tgtgtttcac ttacctataa accaaagggg aaatggtatt gcccaaagtg
841 caggggagat aatgagaaaa caatggacaa aagtactgaa aagacaaaaa aggatagaag
901 atcgaggtag taaaggccat ccacatttta aagggttatt tgtcttttat ataattcggt
961 tgcctttcaga aaatgtttta gggtaaagtc ataagactat gcaataattt ttaatcatta
1021 gtattaatgg tgtattaaaa gttgtgttac tttgaaaaaa aaaaaaaaaa aaaaaaaaaa
    
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SEQ ID NO:3 Primer MLGQQQQQ

SEQ ID NO:4 Primer KKDRRSR

SEQ ID NO:5 peptide 7-26 of p33ING2 (KMP1)

QQLYSSAALLTGERSRL LTC

SEQ ID NO:6 missense amino acid or nucleic acid sequence – arg 153 to ser

1 MLGQQQQQLY SSAALLTGER SRLLTCTVQD YLECVESLPH DMQRNVSVLR
51 ELDNKYQETL KEIDDVYEKY KKEDDLNQKK RLQQLLQRAL INSQELGDEK
101 IQIVTQMLEL VENRARQMEL HSQCFQDPAE SERASDKAKM DSSQPERSSR
151 RPSRQRTSES RDLCHMANGI EDCDDQPPKE KKSksAKKKK RSKAKQEREA
201 SPVEFAIDPN EPTYCLCNQV SYGEMIGCDN EQCPIEFWFH SCVSLTYKPK
251 GKWYCPKCRG DNEKTMDKST ETKTKDRRSR

SEQ ID NO:7 p33ING2 genomic DNA sequence (Exon1/Intron)

(GenBank Accession No. HSING2S1)

Exon 1: 1..239

Intron: 240...>423

1 gcggccgcgg ccggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcggat
61 cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg
121 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt
181 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaagg
241 taggggccgc ggggctgccg gcctcgggag ccggtggcgg ggagcctgtc cgggggagtg
301 ccaccttccc tttctcccgt gacagtctcc ccgagcgcac cgaggggtctg ccgagcggga
361 ctgggaggac tggagaccgg gttggcggcc ctccgtggcc ccgcggtggg cgagtgaagg
421 aga

SEQ ID NO:8 p33ING1 amino acid sequence

p33ING1 Length: 279

1 MLSPANGEQL HLVNYVEDYL DSIESLPFDL QRNVSLMREI DAKYQEILKE
51 LDECYERFSR ETDGAQKRRM LHCVRALIR SQELGDEKIQ IVSQMVOLVE
101 NRTRQVDHSV ELFEAQQLG DTAGNSGKAG ADRPKGEAAA QADKPNKRS
151 RRQRNNENRE NASSNHDHDD GASGTPKEKK AKTSKKKKRS KAKAEREASP
201 ADLPIDPNP TYCLCNQVSY GEMIGCDNDE CPIEFWFHSC VGLNHKPKGK
251 WYCPKCRGEN EKTMDKALEK SKKERAYNR

SEQ ID NO:9 Peptide 1-17 and C of p33ING1 (KMP2)

MLSPANGEQLHLVNYVEC

SEQ ID NO:10 p33ING2 genomic DNA sequence (Exon 2/intron)

(GenBank Accession No. HSING2S2)

Intron: <1..123

Exon 2: 124..938

1 ccaaagagga gtatggtttc atggtttgag ttctaatttc aattctgtaa aaaataacta
 61 ccttggaat gttgtgtctg ctaacacatg ataacgttct catttttctt ttcctttttt
 121 tagaaacggt aaaggaaatt gatgatgtct acgaaaaata taagaaagaa gatgatttaa
 181 accagaagaa acgtctacag cagcttctcc agagagcact aattaatagt caagaattgg
 241 gagatgaaaa aatacagatt gttacacaaa tgctcgaatt ggtggaaaat cgggcaagac
 301 aaatggagtt acactcacag tgtttccaag atcctgctga aagtgaacga gcctcagata
 361 aagcaaagat ggattccagc caaccagaaa gatcttcaag aagaccccg caggcagcgg
 421 ccagtgaag ccgtgattta tgtcacatgg caaatgggat tgaagactgt gatgatcagc
 481 cacctaaaga aaagaaatcc aagtcagcaa agaaaaagaa acgctccaag gccaaagcagg
 541 aaaggggaagc ttcacctgtt gagtttgcaa tagatcctaa tgaacctaca tactgcttat
 601 gcaaccaagt gtcttatggg gagatgatag gatgtgacaa tgaacagtgt ccaattgaat
 661 ggtttcactt ttcattgtgt tcacttacct ataaaccaa ggggaaatgg tattgcccaa
 721 agtgcagggg agataatgag aaaacaatgg acaaaagtac tgaaaagaca aaaaaggata
 781 gaagatcgag gtagtaaagg ccatccacat tttaaagggt tatttgtctt ttatataatt
 841 cgtttgcttt cagaaaatgt tttagggtaa atgcataaga ctatgcaata atttttaatc
 901 attagtatta atggtgtatt aaaagttgtt gtactttgtc tgtgacctta atttctgca
 961 ctgagttacc aaat